



RECEIVED

NOV 29 2000

SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Zuker, Charles
Adler, Jon Elliot
Lindemeier, Juergen
The Regents of the University of California

<120> Assays for Sensory Modulators Using a Sensory Cell
Specific G-Protein Beta Subunit

<130> 02307E-092710US

<140> US 09/492,029

<141> 2000-01-26

<150> US 60/117,404

<151> 1999-01-27

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 156

<212> DNA

<213> Rattus sp.

<220>

<223> rat tongue circumvallate papillae taste receptor
cell cDNA clone 165-17

<400> 1

aacaaaaggg cataaagaaa gtggctggga gggagccagg atactaggag tgacacctat 60
agtcatgggc tgagcgctct ggccattccc argccggaca aaggctgctg gtagcccagg 120
agtcatctag ggtggggagg gtctgttctt gtttat 156

<210> 2

<211> 1520

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (78) .. (2000)

<223> rat taste cell specific G-protein beta 3 subunit
(TC-Gbeta3)

<400> 2

gggcgcctgg gaagcggaag cctgggagaa atccagctag agcccaagag ccaggactac 60

cccttgacct gtgaacc atg ggg gag atg gag cag ctg aag cag gag gcg 110
Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala
1 5 10

gag cag ctc aag aag cag att gct gat gcc agg aaa gcc tgt gcg gac 158
Glu Gln Leu Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp
15 20 25

RECEIVED

NOV 28 2000

TECH CENTER 1600/2900

RECEIVED

DEC 04 2000

TECH CENTER 1600/2900

atc act ctg gct gag ctt gtg tct ggc ctg gag gtg gtg gga cga gtc	206
Ile Thr Leu Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val	
30 35 40	
cag atg cgg aca cgg agg acg tta agg gga cac ctg gct aag atc tat	254
Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr	
45 50 55	
gcc atg cac tgg gcc act gac tct aag ctg cta gta agt gcc tcg cag	302
Ala Met His Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln	
60 65 70 75	
gat ggg aag ctg atc gtg tgg gac act tac acc acc aat aag gtg cat	350
Asp Gly Lys Leu Ile Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His	
80 85 90	
gct atc ccg ctg cgt tcc tcc tgg gtc atg acc tgt gcc tat gca cca	398
Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro	
95 100 105	
tca ggg aac ttc gtg gca tgt ggg ggg cta gat aac atg tgc tca atc	446
Ser Gly Asn Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile	
110 115 120	
tac agc ctc aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gaa ctc	494
Tyr Ser Leu Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu	
125 130 135	
tcg gct cac aca ggt tat ctc tcc tgt tgc cgc ttc ctg gat gac aac	542
Ser Ala His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn	
140 145 150 155	
aac att gtg act agc tct ggg gac acc acg tgt gcc ttg tgg gac att	590
Asn Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile	
160 165 170	
gag acg ggg cag cag aag aca gtg ttc gtg gga cac act ggt gac tgc	638
Glu Thr Gly Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys	
175 180 185	
atg agc ctg gct gtg tcc cca gac tac aaa ctc ttc atc tcg gga gct	686
Met Ser Leu Ala Val Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala	
190 195 200	
tgt gat gcc agc gcc aag ctc tgg gat gtg agg gaa ggg acc tgt cgc	734
Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg	
205 210 215	
cag act ttc act ggc cac gag tca gac atc aat gct atc tgt ttc ttt	782
Gln Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe	
220 225 230 235	
ccc aat ggg gag gcc atc tgc act ggc tca gat gat gcc tcc tgc cgc	830
Pro Asn Gly Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg	
240 245 250	
ctc ttt gac ctg agg gca gac cag gaa ctg aca gcc tac tcc cac gag	878
Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu	
255 260 265	

a!
ant.

agc atc atc tgt ggc atc acg tcc gta gcc ttc tca ctc agt ggt cgc 926
 Ser Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg
 270 275 280

ctg ctc ttt gct ggc tat gat gac ttc aac tgc aat gtc tgg gac tct 974
 Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
 285 290 295

ctg aag tgt gag cgt gta ggc gtt ctt tct ggc cat gac aac aga gtc 1022
 Leu Lys Cys Glu Arg Val Gly Val Leu Ser Gly His Asp Asn Arg Val
 300 305 310 315

agt tgc ctg ggg gtc aca gct gac ggc atg gct gtg gcc act gga tcc 1070
 Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser
 320 325 330

tgg gac agc ttc ctc aag atc tgg aac tgaggaggct ggaggaagag 1117
 Trp Asp Ser Phe Leu Lys Ile Trp Asn
 335 340

gtgggaagcc atgaaggctc tcagctgact cctatgccct gtctccttag ggtagctctt 1177

ctataccctg gggccactcc cagtaaactt ccttctaagg gcagggtggga ttataggagt 1237

gtgccttttg gagtagcagg gtcacaaggg caaagaactg cccatttcc tccagggcct 1297

ctcctctcca cagtcctcat agcttctccc ttcataaaca agaacagacc ctccccaccc 1357

tagatgactc ctgggctacc agcagcgttt gtccggcctg ggaatggcca gagcgctcag 1417

cccatgacta taggtgtcac tccatgtatc ctggctccct cccagcgact ttctttctgc 1477

ccttttgttc tctcttatta cctaataaaa tgtagcatcc tgg 1520

<210> 3

<211> 340

<212> PRT

<213> Rattus sp.

<400> 3

Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala Glu Gln Leu Lys Lys
 1 5 10 15

Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Ile Thr Leu Ala Glu
 20 25 30

Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
 35 40 45

Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
 50 55 60

Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
 65 70 75 80

Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
 85 90 95

Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
 100 105 110

Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Ser Leu Lys Ser
115 120 125

Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
130 135 140

Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
145 150 155 160

Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
165 170 175

Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
180 185 190

Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
195 200 205

Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
210 215 220

His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
225 230 235 240

Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
245 250 255

Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu Ser Ile Ile Cys Gly
260 265 270

Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
275 280 285

Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Leu Lys Cys Glu Arg
290 295 300

Val Gly Val Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
305 310 315 320

Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
325 330 335

Lys Ile Trp Asn
340

<210> 4
<211> 1523
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (7)..(1029)
<223> human taste cell specific G-protein beta 3 subunit

<400> 4
gggtcg atg ggg gag atg gag caa ctg cgt cag gaa gcg gag cag ctc
Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu
1 5 10

48

aag aag cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg	96
Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu	
15 20 25 30	
gca gag ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg	144
Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg	
35 40 45	
acg cgg cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac	192
Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His	
50 55 60	
tgg gcc act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag	240
Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys	
65 70 75	
ctg atc gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca	288
Leu Ile Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro	
80 85 90	
ctg cgc tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac	336
Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn	
95 100 105 110	
ttt gtg gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc	384
Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu	
115 120 125	
aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac	432
Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His	
130 135 140	
aca ggt tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg	480
Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val	
145 150 155	
acc agc tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg	528
Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly	
160 165 170	
cag cag aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg	576
Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu	
175 180 185 190	
gct gtg tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc	624
Ala Val Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala	
195 200 205	
agt gcc aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc	672
Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe	
210 215 220	
act ggc cac gag tcg gac atc aac gcc atc tgt ttc ttc ccc aat gga	720
Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly	
225 230 235	
gag gcc atc tgc acg ggc tcg gat gac gct tcc tgc cgc ttg ttt gac	768
Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp	
240 245 250	

a!
cont

ctg cgg gca gac cag gag ctg atc tgc ttc tcc cac gag agc atc atc 816
 Leu Arg Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile
 255 260 265 270
 tgc ggc atc acg tcc gtg gcc ttc tcc ctc agt ggc cgc cta cta ttc 864
 Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe
 275 280 285
 gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc atg aag tct 912
 Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser
 290 295 300
 gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg agc tgc ctg 960
 Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu
 305 310 315
 gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc tgg gac agc 1008
 Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser
 320 325 330
 ttc ctc aaa atc tgg aac tgaggaggct ggagaaaggg aagtggaagg 1056
 Phe Leu Lys Ile Trp Asn
 335 340
 cagtgaacac actcagcagc cccctgcccg accccatctc attcaggtgt tctcttctat 1116
 attccgggtg ccattcccac taagctttct cctttgaggg cagtggggag catgggactg 1176
 tgcctttggg aggcagcatc agggacacag gggcaaagaa ctgccccatc tcttcccatg 1236
 gccttccctc cccacagtcc tcacagcctc tcccttaatg agcaaggaca acctgcccct 1296
 cccagccct ttgcaggccc agcagacttg agtctgaggc cccaggccct aggattcctc 1356
 cccagagcc actacctttg tccaggcctg ggtggtatag ggcgtttggc cctgtgacta 1416
 tggctctggc accactaggg tcttggccct cttcttattc atgctttctc ctttttctac 1476
 ctttttttct ctcctaagac acctgcaata aagtgtagca ccctgggt 1523

<210> 5
 <211> 340
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Gly Glu Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys
 1 5 10 15
 Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu
 20 25 30
 Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
 35 40 45
 Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
 50 55 60
 Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
 65 70 75 80

Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
85 90 95

Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
100 105 110

Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser
115 120 125

Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
130 135 140

Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
145 150 155 160

Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
165 170 175

Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
180 185 190

Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
195 200 205

Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
210 215 220

His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
225 230 235 240

Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
245 250 255

Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile Cys Gly
260 265 270

Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
275 280 285

Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser Glu Arg
290 295 300

Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
305 310 315 320

Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
325 330 335

Lys Ile Trp Asn
340